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FROM FIG 1A2

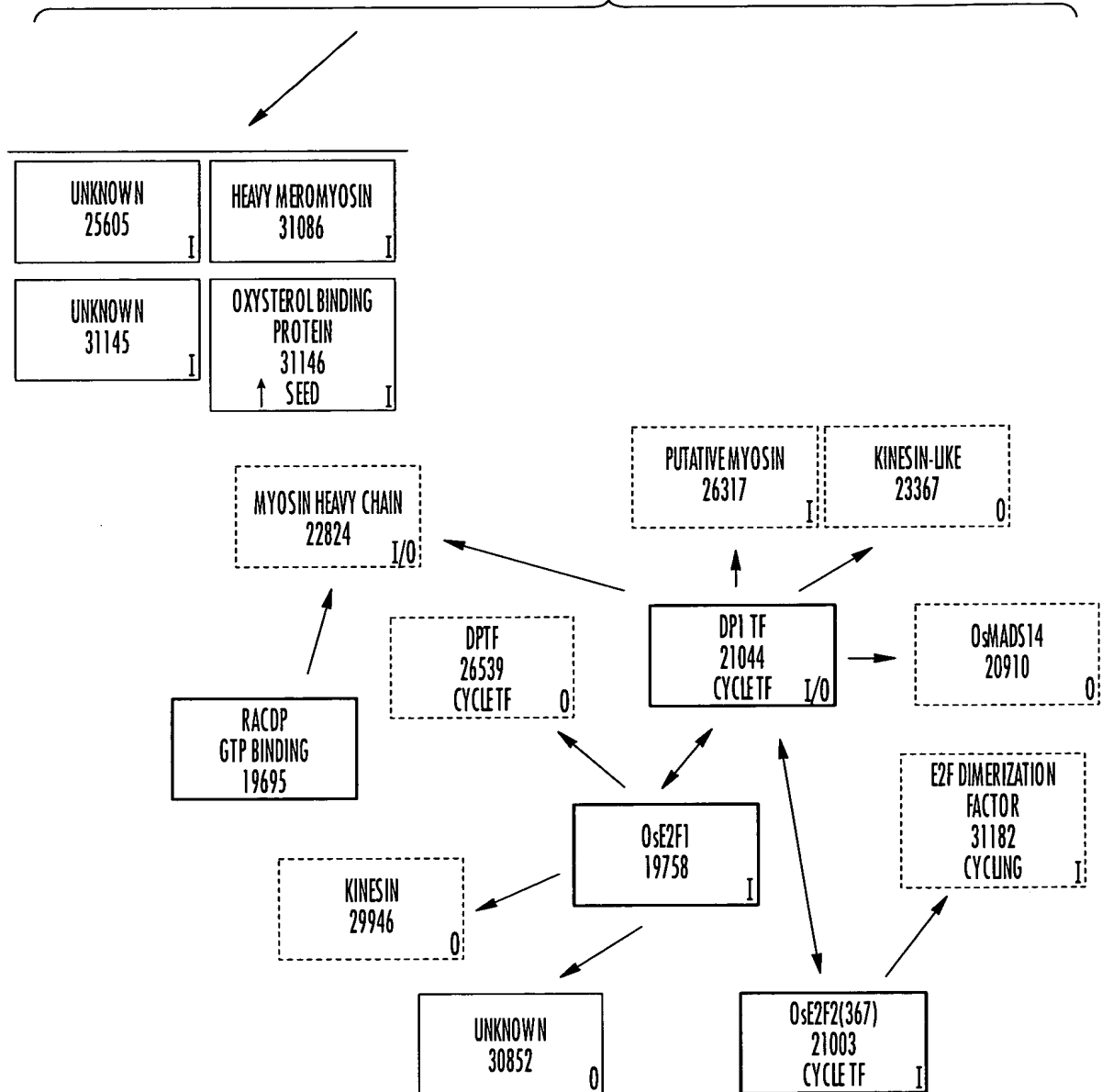
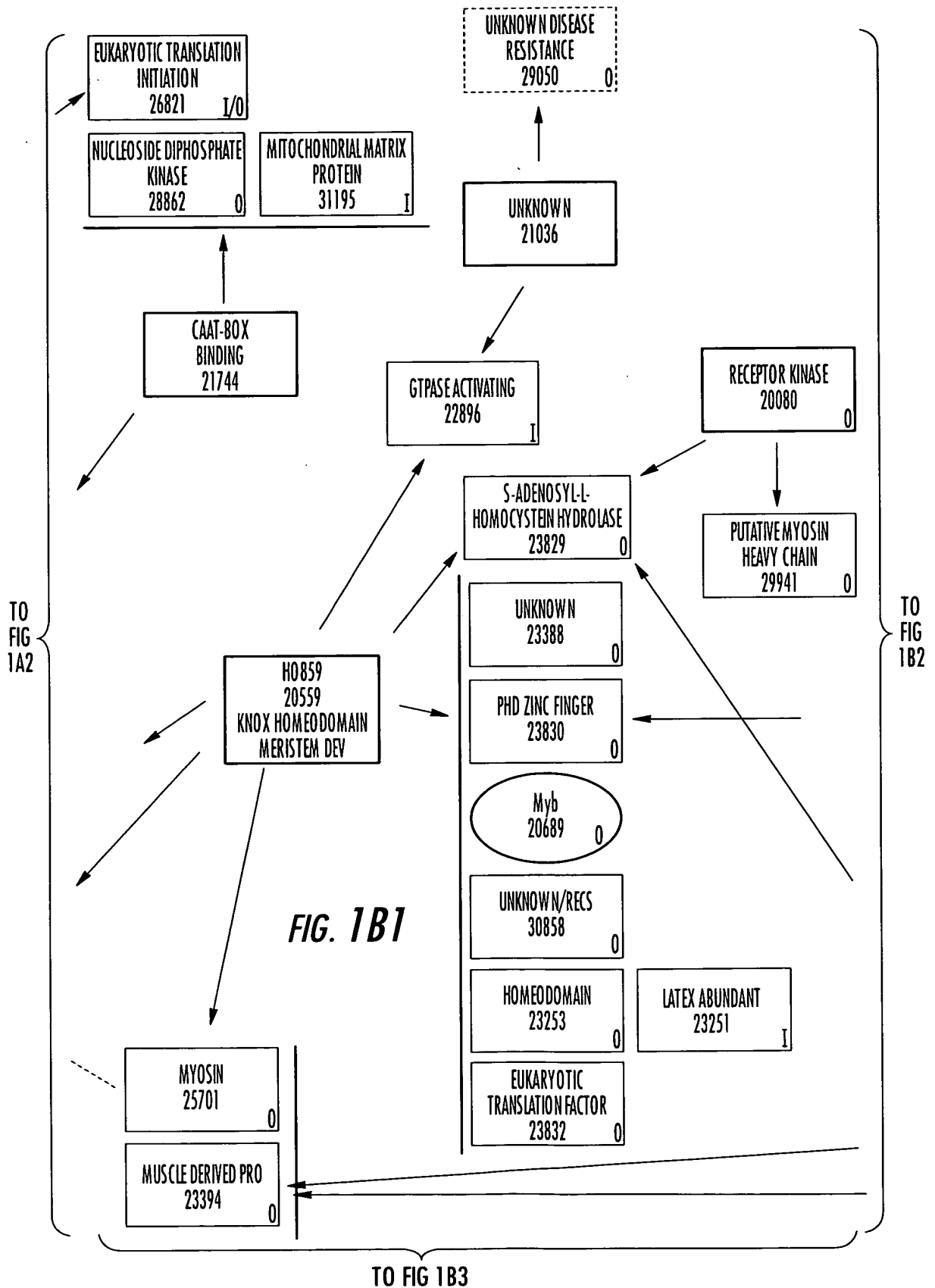


FIG. 1A3

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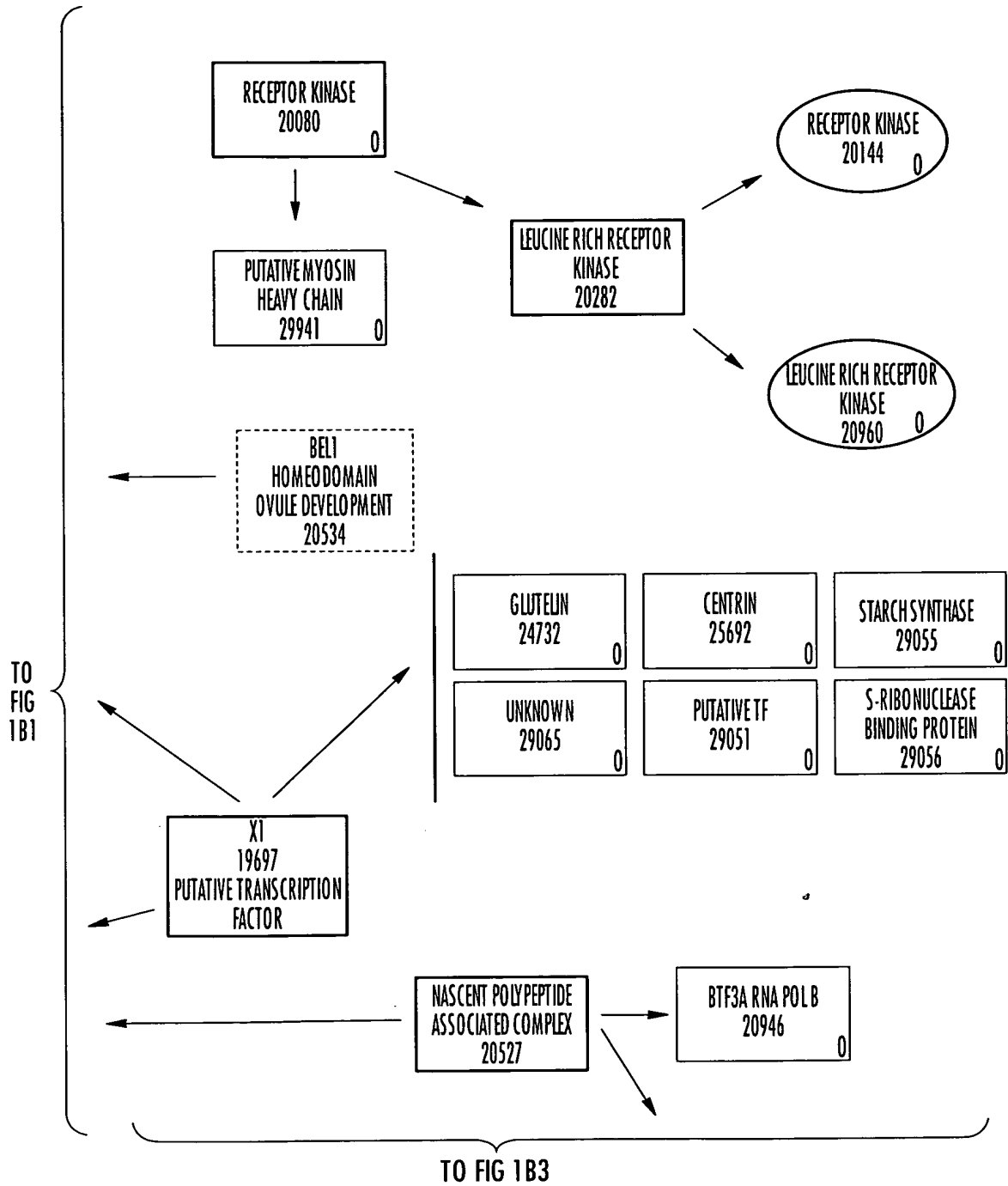


FIG. 1B2

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TO FIG 1B1 AND 1B2

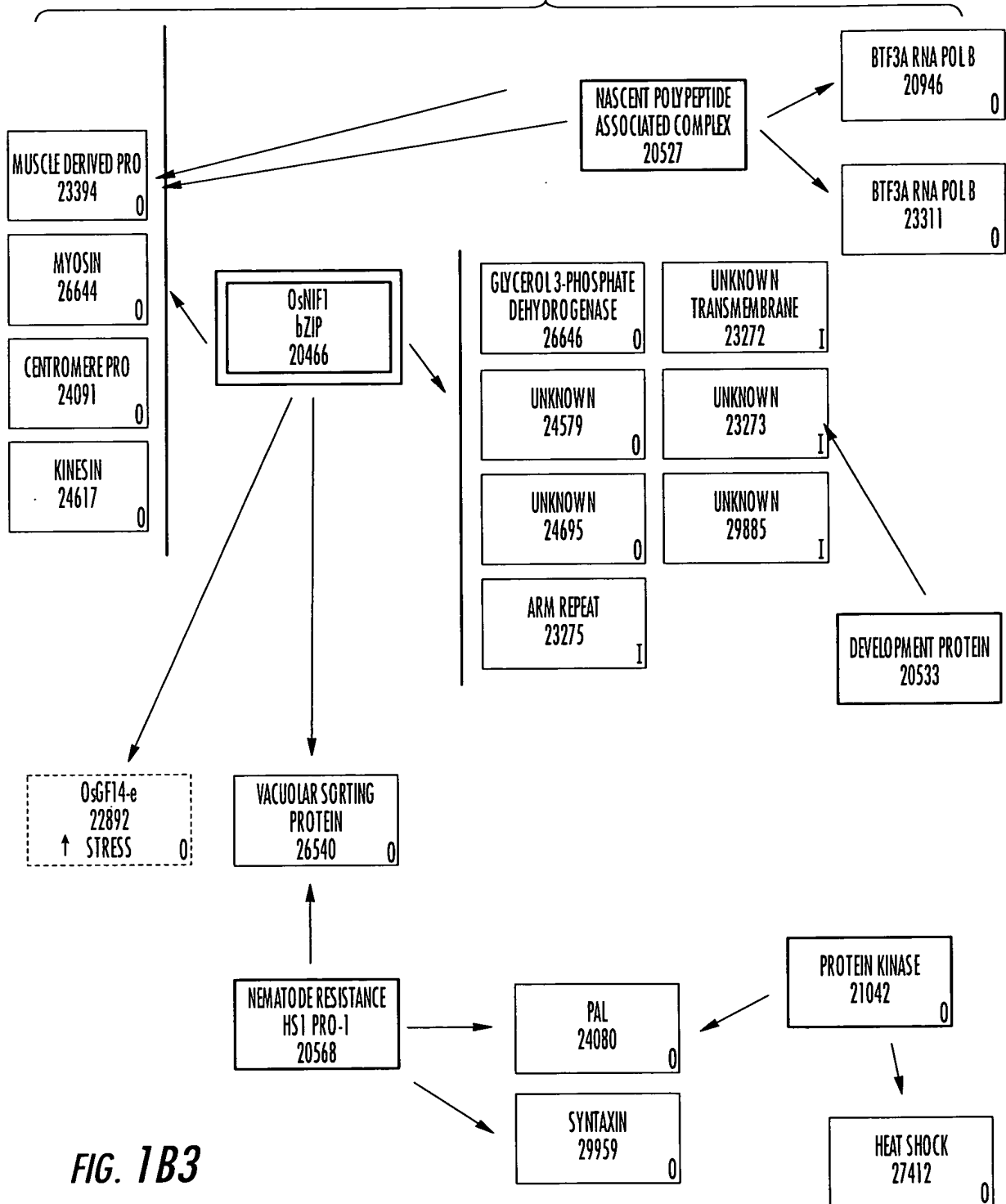
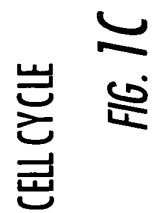
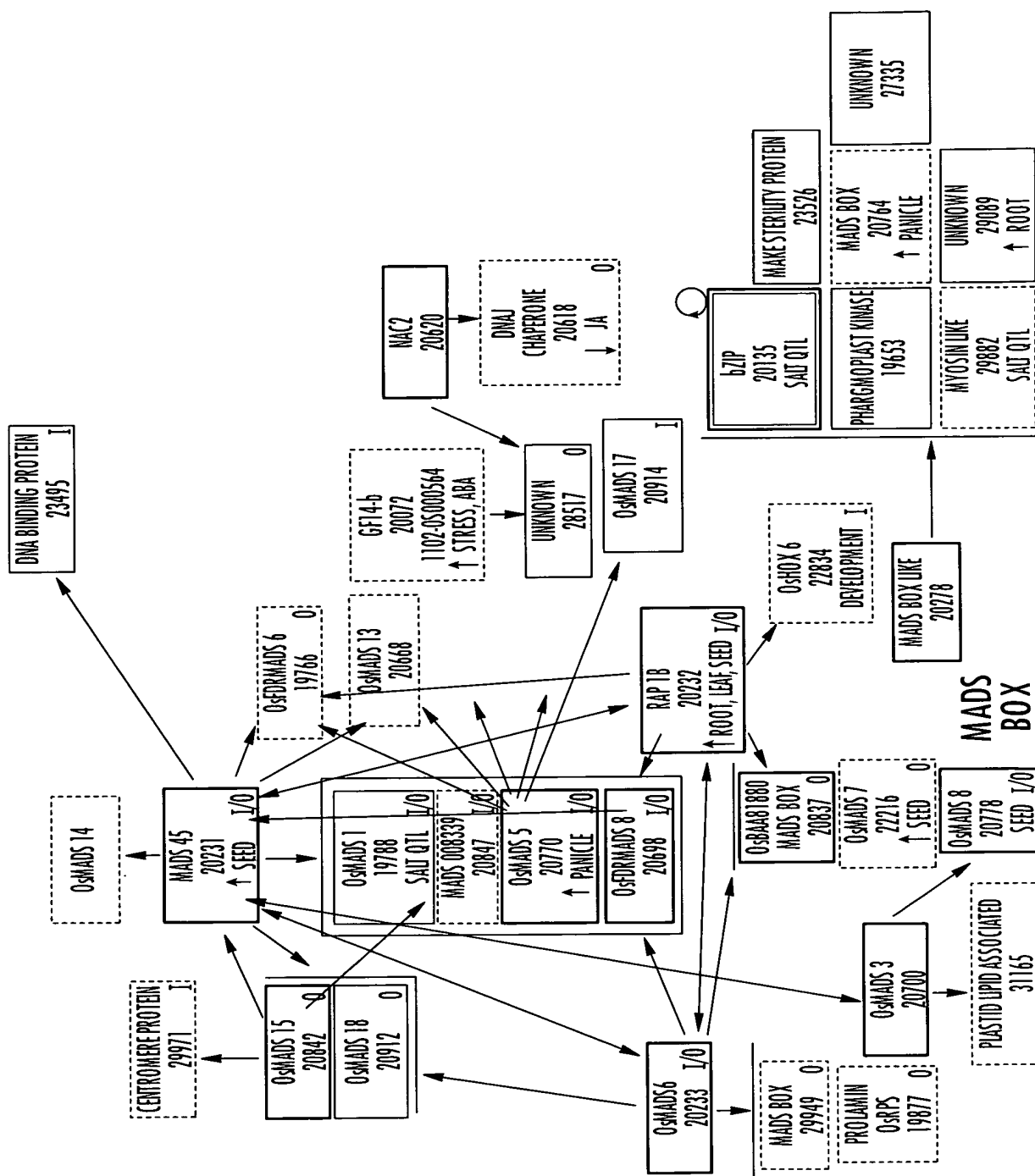


FIG. 1B3





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CONS.	10	20	30	40	50	60	70
	-----MGRGRVELKRIENKINRQVTGSKRRNGLLKKAYELSVLCDAEVALIIFSSRGKLYEFASSS						
19766	-----MGRGKVQLKRIENTINRQVTFSKRRSGLLKKANEISVLCDAEVALIIFSTKGKLYKYATDS						
19788	-----MGRGKVELKRIENKISRQVTFAKRRNGLLKKAYELSLCDAEVALIIFSGRGLFEFSSSS						
20231	-----MGRGRVELKRIENKINRQVTFAKRRNGLLKKAYELSVLCDAEVALIIFSNRGKLYEFCSTQ						
20232	-----MGRGKVQLKRIENKINRQVTFSKRRSGLLKKANEISVLCDAEVALIIFSTKGKLYEYATDS						
20233	-----MGRGRVELKRIENKINRQVTFSKRRNGLLKKAYELSVLCDAEVALIIFSSRGKLYEFGSAG						
20278	-----MGRGKIEIKRIENATNRQVTYSKRRTGIMKKARELTVLCDAQVAIIMFSSTGKYHEFCSPS						
20668	-----MGRGRIEIKRIENTTSRQVTFCKRRNGLLKKAYELSVLCDAEVALIIVFSSRGRLYEYSNNN						
20698	MV-----RGRTELKRIENPTSRQVTFSKRRNGLLKKAFELSVLCDAEVALIIVFSPRGRLYEFASAP						
20700	-----MGRGKIEIKRIENTTNRQVTFCKRRNGLLKKAYELSVLCDAEVALIIVFSSRGRLYEYANNS						
20770	-----MGRGKVELKRIENKISRQVTFAKRRNGLLKKAYELSVLCDAEVALIIFSTRGRLFEFSTSS						
20778	-----MGRGRVELKRIENKINRQVTFAKRRNGLLKKAYELSVLCDAEVALIIFSNRGKLYEFCSGQ						
20837	MA-----RERREIKRIESAAARQVTFSKRRRGLFKKAEELSVLCDAEVALIIVFSSTGKLSHFAS-S						
20842	-----MGRGKVQLKRIENKINRQVTFSKRRNGLLKKAEISVLCDAEVAIVFSPKGKLYEYATDS						
20847	EGEG--RAATGKRERIAIRRIDNLAARQVTFSKRRRGLFKKAEELSILCDAEVLVVSATGKLFQFAS-T						
20910	-----MGRGKVQLKRIENKINRQVTFSKRRSKLLKKANEISVLCDAEVALIIFSTKGKLYEYATDS						
20912	-----MGRGPVQLRRIENKINRQVTFSKRRNGLLKKAEISVLCDAEVALIIVFSTKGKLYEFSHS						
20914	-----MGRGRVELKRIENKINRQVTFSKRRNGLLKKAYELSVLCDAEVALIIFSSRGKLYEFGSAG						
21116	LVGGSWRSIGMGRGRVELKRIENKINRKVTFAKRRNGLLKKAYELSVLCDAEVALIIFSNRGKLYEFCSTQ						
29949	-----MGRGKIVIRRIDNSTSRQVTFSKRRNGLLKKAKELSILCDAEVLVVSSTGXLYEFSST-						

FIG. 3A

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CONS.	80	90	100	110	120	130	140
	S-MTKTLERYQRYSYA--ESAVISAESETQGSWYQEYILKLKAKVEALQKTQRH-----LLGEDLESLSLKLQ						
19766	C-MDKILERYERYSYAEK--VLISAESDTQGNWCHEYRKILKAKVETIQKCQKH-----LMGEDLESNLKLQ						
19788	C-MYKTLERYRSCNYN---SQDAAAPENEI--NYQEYILKLKTRVEFLQTTORN-----ILGEDLGPLSMKELE						
20231	S-MTKTLEKYQKCSYAGPETAQNRESEQLKASRNEYILKLKARVENLQRTORN-----LLGEDLDSLGIKELE						
20232	C-MDKILERYERYSYA--EKVLISAESDTQGNWCHEYRKILKAKVETIQKCQKH-----LMGEDLESNLKLQ						
20233	G-ITKTLERYQHCCYNAQDSNNALS--ET-QSWYHEMSKLKAKFEALQRTQRH-----LLGEDLGPLSVKLQ						
20278	DIKGIFDRYQ-----QAIGTSLWIEQYENMQRTLSHLKDINRNLRTAIRQRMGEDLDGLEFDEL						
20668	N-VKATIDRYKKAHACGSTSGAPLIEVNAQYYQESAKLRHQIQMLQNTNKH-----LVGDNVSNLSLKLK						
20698	S-LQKTIDRYKAYTKDHVNNKTIQDDIQVK---DDTLGLAKKLEALDESRRK-----ILGENLEGCSIEELR						
20700	--VKSTVERYKKANS-DTNSGTVAEVNAQHY-QQESSKLQQISSLQANANSR-----TIVGDSINTMSLRDLK						
20770	C-MYKTLERYRSCNYNLNSCEASAALETEL-SNVQEYILKLKTRVEFLQTTORN-----LLGEDLVPLSLKELE						
20778	S-MTRTLERYQKFSYGGPDTAIQNKENELVQSSRNEYILKLKARVENLQRTORN-----LLGEDLGTLGIKELE						
20837	S-MNEIIDKYNTHSNLGAEPSPDLNLEHS--K-YAHLNEQLAEASLRLRQ-----MRGEELEGLSIDELQ						
20842	R-MDKILERYERYSYA--EKALISAESESEGNWCHEYRKILKAKIETIQKCQKH-----LMGEDHESNLKLQ						
20847	S-MEQIIDRYNSHKTQRAEPSQDLQGEDS--STCARLKEELAETSRLRQ-----MRGEELHRLNVEQLQ						
20910	C-MDKILERYERYSYA--EKVLISAESDTQGNWCHEYRKILKAKVETIQKCQKH-----LMGEDLESNLKLQ						
20912	S-MEGILERYQRYSPD--ERAVLEPNTEDQENWGDEYGILKSKLDALQKSQRQ-----LLGEQLDTLTTKELQ						
20914	G-INKTLEKYNSCCYNAQGSNSALAGGEH-QSWYQEMSRLKTKLECLQRSQRH-----MLGEDLGPLSIKELQ						
21116	S-MTKTLEKYQKCSYAGPETAQNRESEQLKASRNEYILKLKARVENLQRTORN-----LLGPDLDLSLGIKELE						
29949	N-MKTVIDRYTNAKEELLGGNAT---SEIKIWOREAASLRQQLH-NLQESHKQ-----LMGEELSGLGVRDLQ						

FIG. 3B

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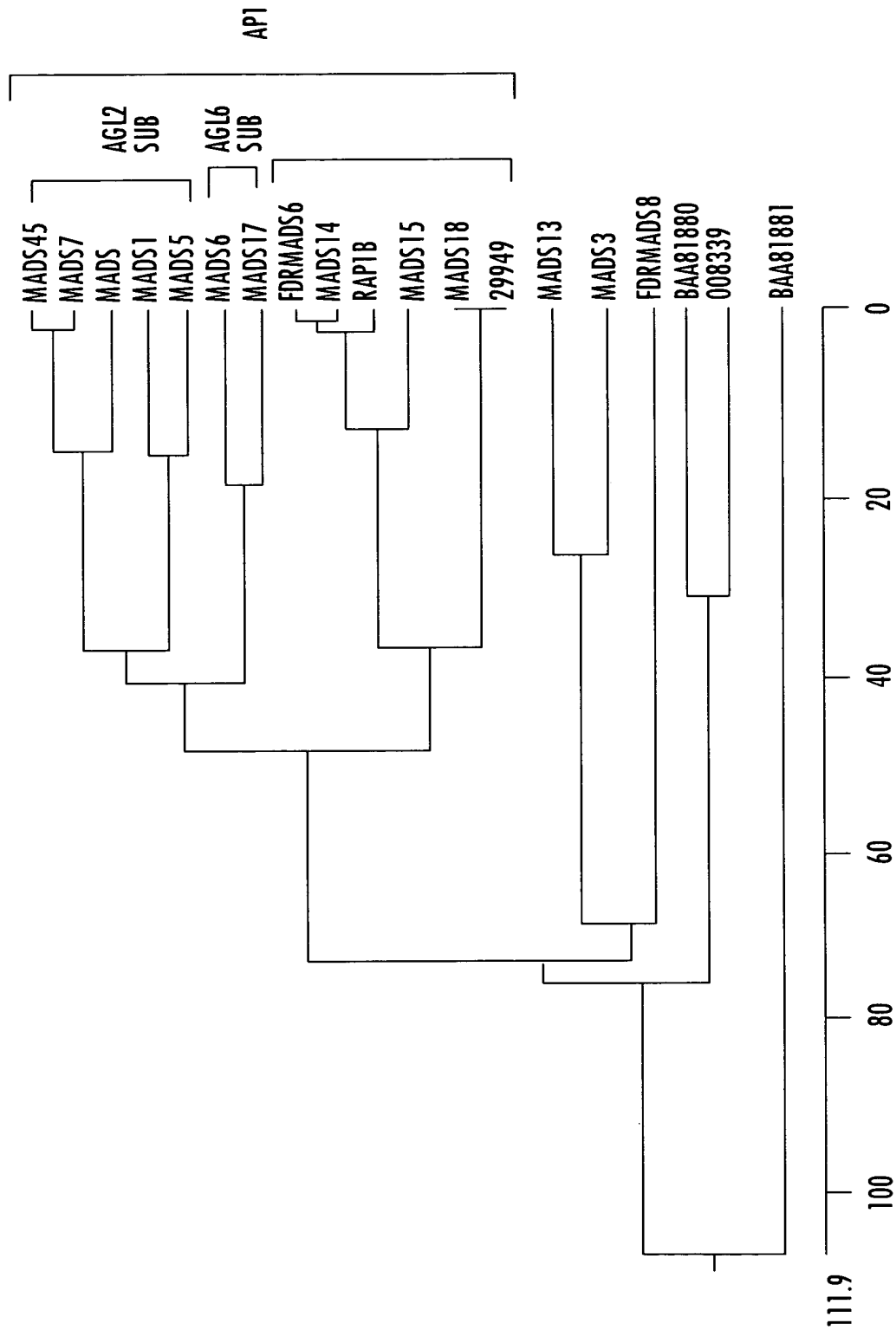
CONS.	150	160	170	180	190	200	210
	QLEKQLESSLKHRSRKTQLLLEQISELQKEKSLQEENKVLQKKLVETEK---GQQVQQQG-WDQGGQTP						
19766	QLEQQLENSLKHRSRKSQMLMESINELQKEKSLQEENKVLQKELVEKQK----VQKQQ-VQWDQTPQT-						
19788	QLENQIEVSLKQIRSRKNQALLDQLFDLKSKEQQLQDLNKLDRKKLQETS-----AENVLHMSWQDGGHSGS						
20231	SLEKQLDSSLKHVRTTRTKHLVDQLTQLQKEQMVSEANRCLRRKLEESNHVR-GQQVWEQGCNLIYERQP						
20232	QLEQQLENSLKHRSRKSQMLMESINELQKEKSLQEENKVLQKELVEKQK----VQKQQQLQ-WDQTPQT-						
20233	QLEKQLECALSQARQKTQLMMEQVEELRRKERQQLGEINRQLKHKLEVEGSTS-NYRAMQQASWAQAVVEN						
20278	GLEQNVDAALKEVRHRKYHVITQTETYKKVKHSYEAYETLQQLGLREEPAFGFVDNTGGWDGGAGAGA						
20668	QLESRLKGIKIRARKNELLASEINYMAREIELQNDNMDLRTKIAEEEQQL-QQVTVARSAAAMELQAAAA						
20698	GLEMKLEKSLHNIRLKKTELLERQIAKLKEKERTL-----LKDNENLR-GKHRNLEAAALVANHMTT						
20700	QVENRLEKGIKIRARKNELLYAEVEYMQREVELQNDNMVYLRKVVENERGQ-QPLNM-----MGAASTSE						
20770	QLENQIEISLMNIRSSKNQQLDQVFELKRKEQQLQDANKDLKRKIQETS-----GENMLHISCQDVGPSG--						
20778	QLEKQLDSSLRHIRSTRTQHMLDQLTDLQRRQMLCEANKCLRRKLEESNQLH-GQ-VWEHGATLLGYERQS						
20837	QLEKNLEAGLHRVMLTKDQQFMEQISELQKSSQLAEENMQLRNQV-----SQ						
20842	QLEQQLESSLKHIISRKSHLMLESISELQKKERSLQEENKALQKELVERQKNV-RGQQQVGQ-WDQTVQQAQ						
20847	ELEKSLESLGSLVLTSSKKILDEIDGLERKRMQLIEENLRLEQV-----SR						
20910	QLEQQLENSLKHRSRKSQMLMESINELQKEKSLQEENKVLQKELVEKQK----VQKQQVQ-WDQTPQT-						
20912	QLEHQLEYSLKHRSKKNQQLLFESISELQKKEKSLKNQNNVLQK-LMETEKEK-NNAIINTN-REEQNGATP						
20914	QLEKQLEYSLSQARQKTQIMMEQVDDLRRKERQQLGELNKLKNKLEAEADSS-NCRSAIQDSWVHGTVVSG						
21116	SLEKQLDSSLKHVRTTRTKHLVDQLTQLQKEQMVSEANRCLRRKLEESNHVR-GQQVWEQGCNLIYERQP						
29949	GLENRLIEISLRNIRMKDNLLKSEIEELHVKGSLIHQENIELSRSLNVMSSQK--LELYNKLQACEQATDAN						

FIG. 3C

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CONS.	220	230	240	250	260	270	280	290
	--A-QQ-PPHSS-F-HREAA--EPTLNIGY---AAGERIA-----Q-----LPP-WML-----							
19766	-----SSSSSFFMMREA---LPTTNISNYPAAAGERIEDVAGQPQ-----HVRIG-LPP--WMLSHING							
19788	STVLADQP-HHHQGLLHPDPDQDHSLSQIGYHHPHAHHQAYMDHLSNEAADMVAAHPNEHIPSGWI-----							
20231	--EVQQ-PLHGGNGFFHPLDAACEPTLQIGY---PAEHHEA-----MNSACMNTYMP-P-WLP-----							
20232	-----ISSSSSFFMMREA---LPTTNISNYPAAAGERIEDVPAGQPQ-----HVRIG-LPP--WMLSHING							
20233	GAAYVQPPPHSA-----AMDSEPTLQIGYPHFVPAEAN-----TIORSTAPAGAENFM-LGWVL-----							
20278	AADMFAFRVPSQPNLHGMAYGGNHDLRL-----G							
20668	AQQQQQNPFVAAAQQLDMKCFPLNLFEEAAQVAVAAQRQQIIPTELNLGYHHHLAIPGATAADAPPPHF--							
20698	TTAPAAWRDVPMTSSTAGAADAMDVETDLYIGLPGTERSSNRSET-----G							
20700	YDHMVNNPY-----DSRNFLOVNIMQQPHYA-----HQLOPTTLQLG-----QQPAFN-							
20770	-----NAS-EANQEFLLH--AICDPSLHIGY-----QAYMDHLNQ-----							
20778	PHAVQQVPPHGGNGFFHSLAAAEPTLQIGF---TPEQ-----MNSCVTAFMPT-WLP-----							
20837	ISPEA--KQVVDTENFVTEGQESVMTALHSGSSQSDNDGDSDVSLKLQ-----LPCGAWK-----							
20842	AQAPQQAQTSSSSSMLRDQQALLPPQNICYPPVMMGERNDAAAAAQAQGVQLRIGGLPP--WMLSHLNA							
20847	MSRNEEMQPGDSEIVYEEGQESVTNASYP--RPPPDNDYSSDTSCLKG-----LHS-----							
20910	-----SSSSSFFMMREA---LPTTNISNYPAAAGERIEDVAGQPQ-----HERIG-LPP--WMLSHING							
20912	STSSPTPVTAADP-----IPTTNNSQSQPRGSEGEAQPSPAAGNSK-----LPP--WMLRTSHT							
20914	GRVLNAQPP--P-----DIDCEPTLQIGY-YQFVRPEAA-----NPRSNGGGDQNNNFV-MGWPL-----							
21116	--EVQQ-PLHGGNGFFHPLDAACEPTLQIGY---PAEHHEA-----MNSACMNTYMPPLP							
29949	--ESSSTPYSFRIIQNANMPPSLELS-QSQQ--REGECSKTA-----APELGL-----HLP							

FIG. 3D



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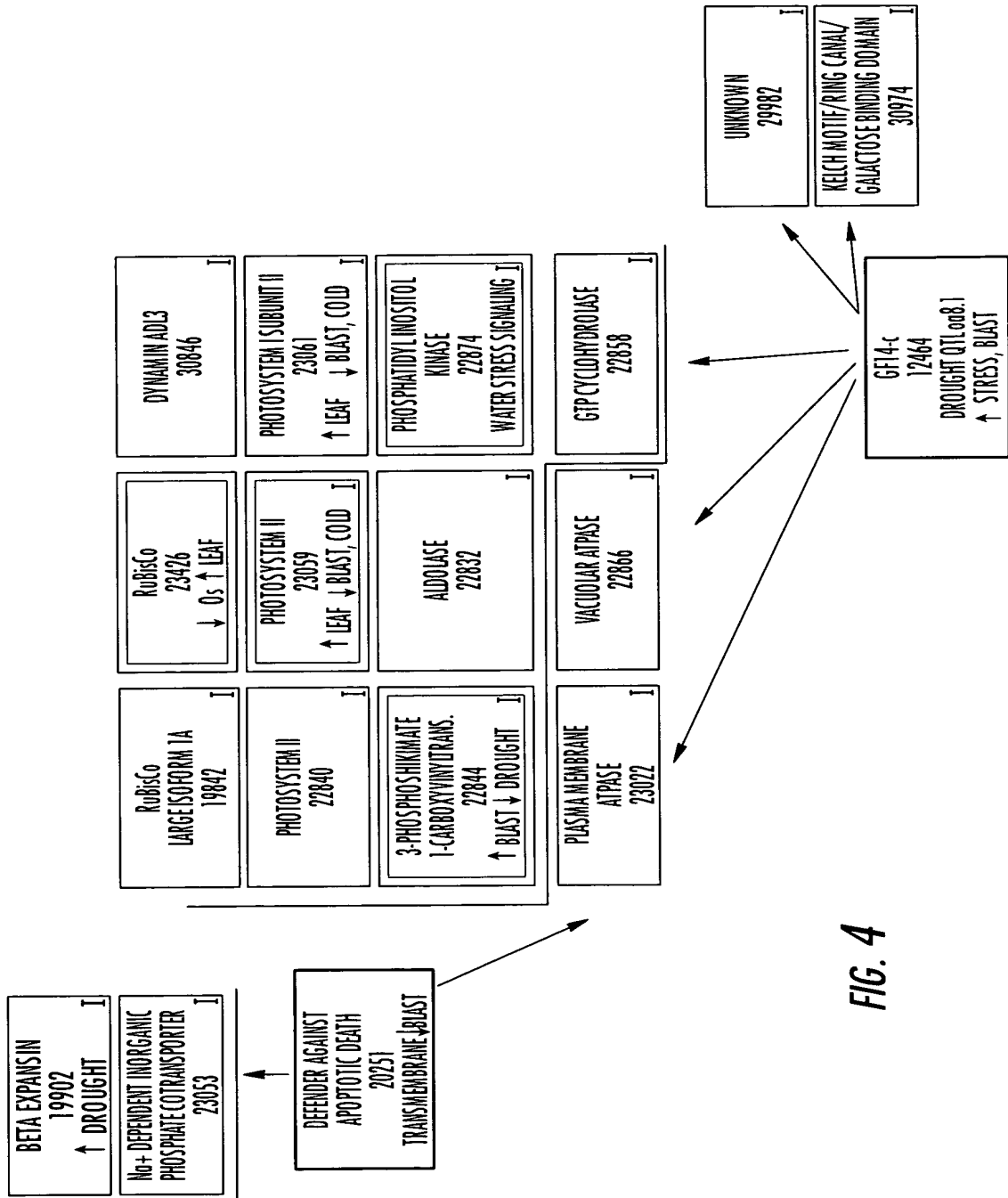


FIG. 4

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CHITINASE AND CELLULOSE SYNTHASE INTERACTIONS

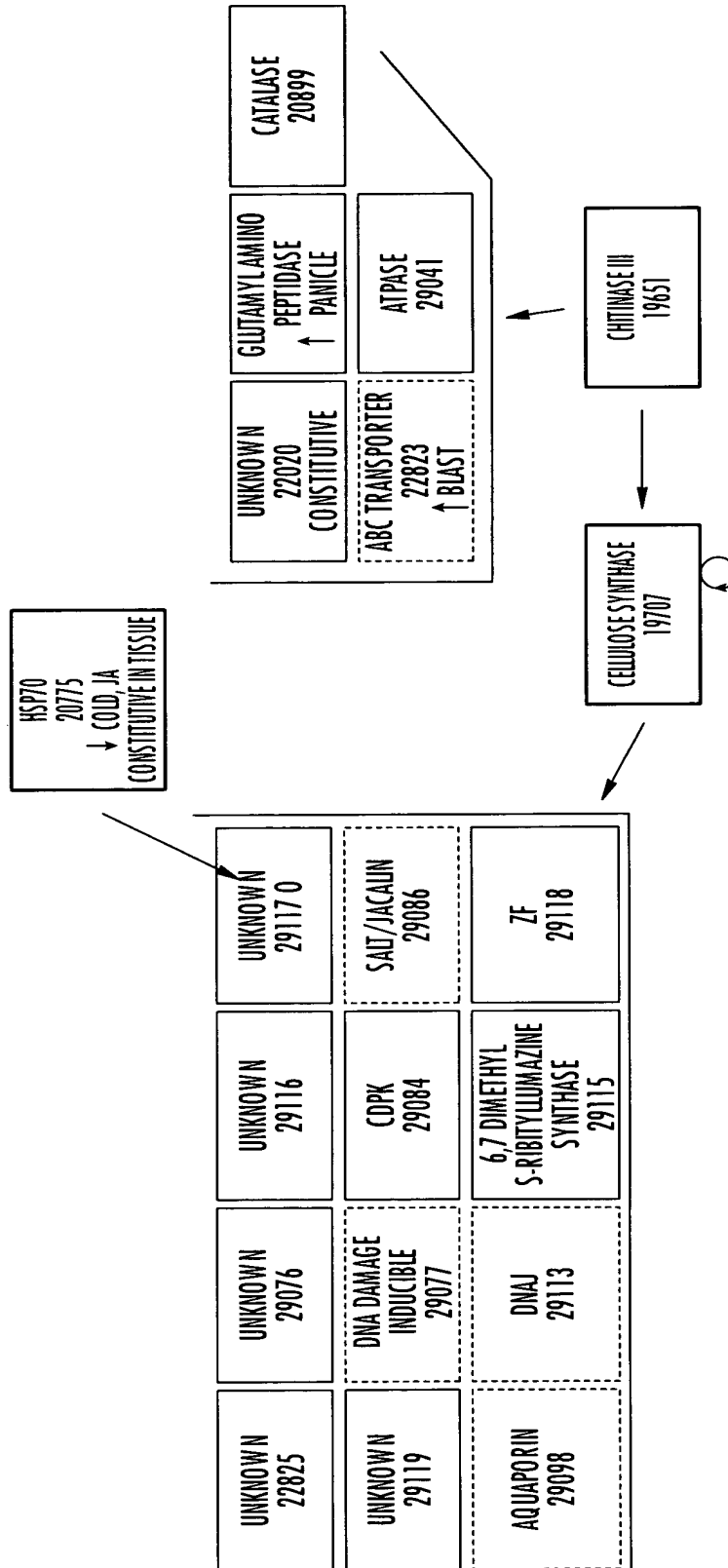


FIG. 5

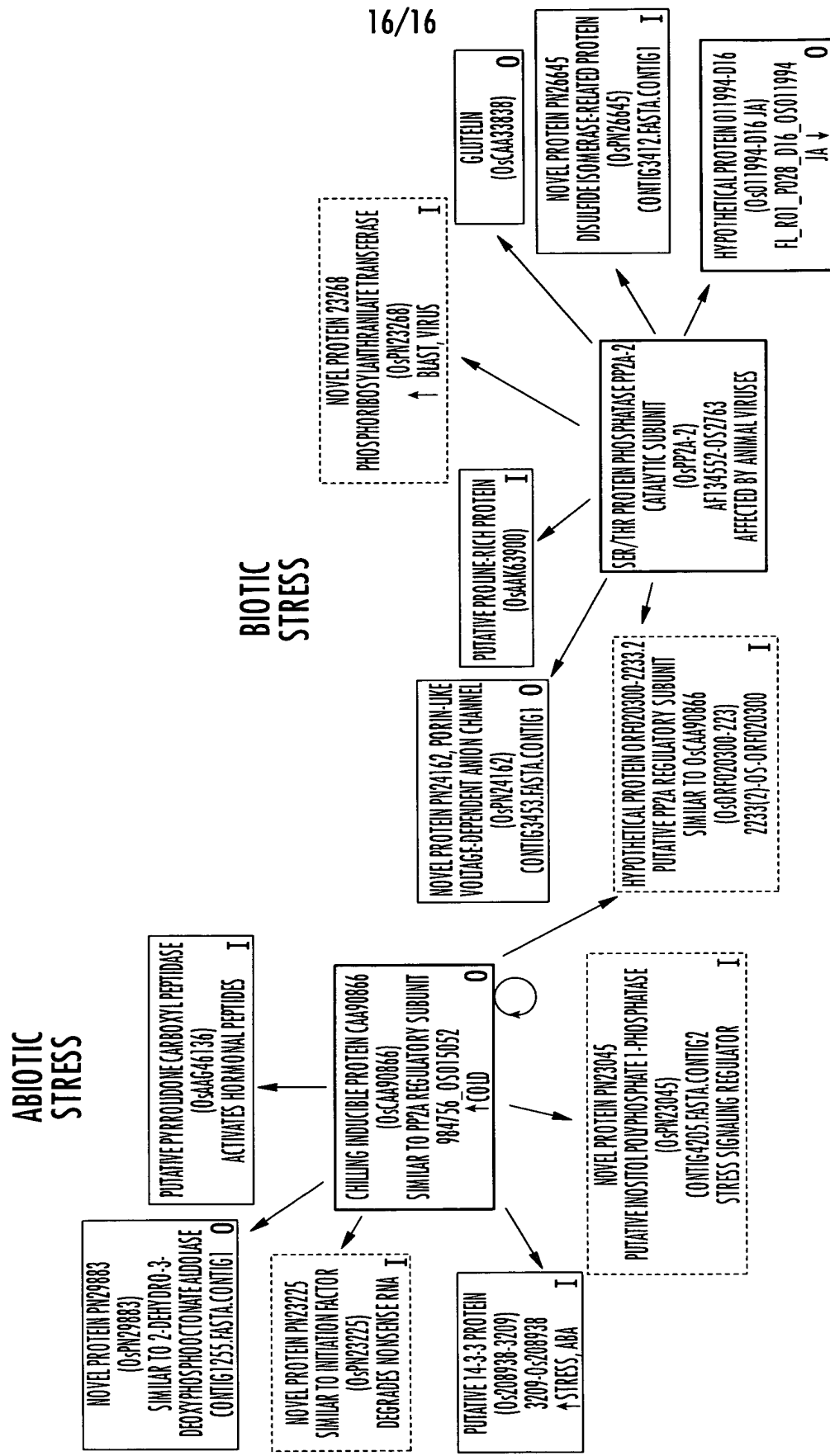


FIG. 6